SEQUENCE LISTING

<110> Glucksman, Maria Alexandra
      Williamson, Mark

<120> 22438, 23553, 25278, and 26212 Novel
  Human Sulfatases

<130> 35800/191890(5800-79

<140> 09/495,823
<141> 2000-01-31

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 525
<212> PRT
<213> homo sapiens

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Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
            20                  25                  30
Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
        35                  40                  45
Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
     50                  55                  60
Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
65                  70                  75                  80
Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
                85                  90                  95
Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
            100                 105                 110
Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
            115                 120                 125
Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
            130                 135                 140
Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
145                 150                 155                 160
Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro
                165                 170                 175
Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
                180                 185                 190
Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
            195                 200                 205
Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
            210                 215                 220
Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
225                 230                 235                 240
```

```
Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
             245                 250                 255
Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
             260                 265                 270
Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
             275                 280                 285
His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly
             290                 295                 300
Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr
305                 310                 315                 320
Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr
             325                 330                 335
Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg
             340                 345                 350
Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile
             355                 360                 365
Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg
             370                 375                 380
Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln
385                 390                 395                 400
Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu
             405                 410                 415
Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr
             420                 425                 430
Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu
             435                 440                 445
Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu
             450                 455                 460
Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro
465                 470                 475                 480
Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp
             485                 490                 495
Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys
             500                 505                 510
Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala
             515                 520                 525
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<210> 2
<211> 2175
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (248)...(1825)

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tacagccccc aacattccta tagccgttat cactgccatc accactgcca ccagcatctt     120
cttgcagatt ccacccctgc tccccagaga cttcctgctt tgaaagtgag cagaaaggaa     180
gctctcagaa aaatctctag tggtggctgc cgtcgctcca gacaatcgga atcctgcctt     240
caccacc atg ggc tgg ctt ttt cta aag gtt ttg ttg gcg gga gtg agt     289
        Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser
          1               5                  10
```

2

```
ttc tca gga ttt ctt tat cct ctt gtg gat ttt tgc atc agt ggg aaa        337
Phe Ser Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys
 15              20              25              30

aca aga gga cag aag cca aac ttt gtg att att ttg gcc gat gac atg        385
Thr Arg Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met
                35              40              45

ggg tgg ggt gac ctg gga gca aac tgg gca gaa aca aag gac act gcc        433
Gly Trp Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala
                50              55              60

aac ctt gat aag atg gct tcg gag gga atg agg ttt gtg gat ttc cat        481
Asn Leu Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His
            65              70              75

gca gct gcc tcc acc tgc tca ccc tcc cgg gct tcc ttg ctc acc ggc        529
Ala Ala Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly
        80              85              90

cgg ctt ggc ctt cgc aat gga gtc aca cgc aac ttt gca gtc act tct        577
Arg Leu Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser
 95              100             105             110

gtg gga ggc ctt ccg ctc aac gag acc acc ttg gca gag gtg ctg cag        625
Val Gly Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln
                115             120             125

cag gcg ggt tac gtc act ggg ata ata ggc aaa tgg cat ctt gga cac        673
Gln Ala Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His
            130             135             140

cac ggc tct tat cac ccc aac ttc cgt ggt ttt gat tac tac ttt gga        721
His Gly Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly
            145             150             155

atc cca tat agc cat gat atg ggc tgt act gat act cca ggc tac aac        769
Ile Pro Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn
    160             165             170

cac cct cct tgt cca gcg tgt cca cag ggt gat gga cca tca agg aac        817
His Pro Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn
175             180             185             190

ctt caa aga gac tgt tac act gac gtg gcc ctc cct ctt tat gaa aac        865
Leu Gln Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn
            195             200             205

ctc aac att gtg gag cag ccg gtg aac ttg agc agc ctt gcc cag aag        913
Leu Asn Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys
            210             215             220

tat gct gag aaa gca acc cag ttc atc cag cgt gca agc acc agc ggg        961
Tyr Ala Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly
```

3

```
agg ccc ttc ctg ctc tat gtg gct ctg gcc cac atg cac gtg ccc tta   1009
Arg Pro Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu
240                 245                 250

ccc gtg act cag cta cca gca gcg cca cgg ggc aga agc ctg tat ggt   1057
Pro Val Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly
255                 260                 265                 270

gca ggg ctc tgg gag atg gac agt ctg gtg ggc cag atc aag gac aaa   1105
Ala Gly Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys
                    275                 280                 285

gtt gac cac aca gtg aag gaa aac aca ttc ctc tgg ttt aca gga gac   1153
Val Asp His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp
                290                 295                 300

aat ggc ccg tgg gct cag aag tgt gag cta gcg ggc agt gtg ggt ccc   1201
Asn Gly Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro
            305                 310                 315

ttc act gga ttt tgg caa act cgt caa ggg gga agt cca gcc aag cag   1249
Phe Thr Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln
    320                 325                 330

acg acc tgg gaa gga ggg cac cgg gtc cca gca ctg gct tac tgg cct   1297
Thr Thr Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro
335                 340                 345                 350

ggc aga gtt cca gtt aat gtc acc agc act gcc ttg tta agc gtg ctg   1345
Gly Arg Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu
                355                 360                 365

gac att ttt cca act gtg gta gcc ctg gcc cag gcc agc tta cct caa   1393
Asp Ile Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln
                370                 375                 380

gga cgg cgc ttt gat ggt gtg gac gtc tcc gag gtg ctc ttt ggc cgg   1441
Gly Arg Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg
            385                 390                 395

tca cag cct ggg cac agg gtg ctg ttc cac ccc aac agc ggg gca gct   1489
Ser Gln Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala
    400                 405                 410

gga gag ttt gga gcc ctg cag act gtc cgc ctg gag cgt tac aag gcc   1537
Gly Glu Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala
415                 420                 425                 430

ttc tac att acc ggt gga gcc agg gcg tgt gat ggg agc acg ggg cct   1585
Phe Tyr Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro
                435                 440                 445

gag ctg cag cat aag ttt cct ctg att ttc aac ctg gaa gac gat acc   1633
```

```
Glu Leu Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr
            450                 455                 460

gca gaa gct gtg ccc cta gaa aga ggt ggt gcg gag tac cag gct gtg    1681
Ala Glu Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val
        465                 470                 475

ctg ccc gag gtc aga aag gtt ctt gca gac gtc ctc caa gac att gcc    1729
Leu Pro Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala
        480                 485                 490

aac gac aac atc tcc agc gca gat tac act cag gac cct tca gta act    1777
Asn Asp Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr
495                 500                 505                 510

ccc tgc tgt aat ccc tac caa att gcc tgc cgc tgt caa gcc gca taa    1825
Pro Cys Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala  *
                515                 520                 525

cagaccaatt tttattccac gaggaggagt acctggaaat taggcaagtt tgcttccaaa    1885
tttcattttt accctcttta caaacacacg ctttagttta gtcttggagt ttagttttgg    1945
agttagcctt gcatatccct tctgtatcct gtccctcctc cacgccgacc cgagagcagc    2005
tgagctgcgc tggctctggg cagggagtgt gccttaatgg gaagcacacg ggctttggag    2065
tcaggcacag gtgccagctc cagcttttga acttgggcaa ttgtttaacc taacctgcaa    2125
gttgattttg agggttaaat aaaggcatac atgaaaaaaa aaaaaaaaaa              2175

<210> 3
<211> 871
<212> PRT
<213> homo sapiens

<400> 3
Met Lys Tyr Ser Cys Cys Ala Leu Val Leu Ala Val Leu Gly Thr Glu
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Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
        20                  25                  30
Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
        35                  40                  45
Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
        50                  55                  60
Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
65                  70                  75                  80
Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
                85                  90                  95
Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
            100                 105                 110
Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
            115                 120                 125
Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
    130                 135                 140
Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145                 150                 155                 160
Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
            165                 170                 175
Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
```

5

```
              180                    185                    190
Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
         195                    200                    205
Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
    210                    215                    220
His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225                    230                    235                    240
Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
                   245                    250                    255
Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
              260                    265                    270
Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
         275                    280                    285
Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
    290                    295                    300
Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305                    310                    315                    320
Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
                   325                    330                    335
Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
              340                    345                    350
Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
         355                    360                    365
Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
    370                    375                    380
Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385                    390                    395                    400
Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
                   405                    410                    415
Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
              420                    425                    430
Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
         435                    440                    445
Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
    450                    455                    460
Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465                    470                    475                    480
Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
                   485                    490                    495
Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
              500                    505                    510
Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
         515                    520                    525
Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
    530                    535                    540
Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545                    550                    555                    560
Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
                   565                    570                    575
His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
         580         0        585                    590
Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
              595                    600                    605
Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
    610                    615                    620
```

6

Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625   630   635   640
Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
                645   650   655
Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
                660   665   670
Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
            675   680   685
Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
        690   695   700
Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705   710   715   720
Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
                725   730   735
Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
            740   745   750
His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
            755   760   765
Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
        770   775   780
Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785   790   795   800
Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
            805   810   815
Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
        820   825   830
Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
        835   840   845
Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
        850   855   860
Leu Trp Asp Gly Trp Glu Gly
865   870

<210> 4
<211> 4321
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (510)...(3125)

<221> misc_feature
<222> 4310
<223> n = A,T,C or G

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cccacgcgtc cggctaatga atcttggggc cggtgtcggg ccggggcggc ttgatcggca 60
actaggaaac cccaggcgca gaggccagga gcgagggcag cgaggatcag aggccaggcc 120
ttcccggctg ccggcgctcc tcggaggtca gggcagatga ggaacatgac tctcccccctt 180
cggaggagga aggaagtccc gctgccacct tatctctgct cctctgcctc ctccctgttc 240
ccagagcttt ttctctagag aagattttga aggcggcttt tgtgctgacg gccacccacc 300
atcatctaaa gaagataaac ttggcaaatg acatgcaggt tcttcaaggc agaataattg 360
cagaaaatct tcaaaggacc ctatctgcag atgttctgaa tacctctgag aatagagatt 420

7

```
gattattcaa ccaggatacc taattcaaga actccagaaa tcaggagacg gagacatttt  480
gtcagttttg caacattgga ccaaataca atg aag tat tct tgc tgt gct ctg  533
                                    Met Lys Tyr Ser Cys Cys Ala Leu
                                     1               5

gtt ttg gct gtc ctg ggc aca gaa ttg ctg gga agc ctc tgt tcg act  581
Val Leu Ala Val Leu Gly Thr Glu Leu Leu Gly Ser Leu Cys Ser Thr
     10                  15                  20

gtc aga tcc ccg agg ttc aga gga cgg ata cag cag gaa cga aaa aac  629
Val Arg Ser Pro Arg Phe Arg Gly Arg Ile Gln Gln Glu Arg Lys Asn
 25                  30                  35                  40

atc cga ccc aac att att ctt gtg ctt acc gat gat caa gat gtg gag  677
Ile Arg Pro Asn Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu
                 45                  50                  55

ctg ggg tcc ctg caa gtc atg aac aaa acg aga aag att atg gaa cat  725
Leu Gly Ser Leu Gln Val Met Asn Lys Thr Arg Lys Ile Met Glu His
             60                  65                  70

ggg ggg gcc acc ttc atc aat gcc ttt gtg act aca ccc atg tgc tgc  773
Gly Gly Ala Thr Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys
         75                  80                  85

ccg tca cgg tcc tcc atg ctc acc ggg aag tat gtg cac aat cac aat  821
Pro Ser Arg Ser Ser Met Leu Thr Gly Lys Tyr Val His Asn His Asn
     90                  95                 100

gtc tac acc aac aac gag aac tgc tct tcc ccc tcg tgg cag gcc atg  869
Val Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala Met
105                 110                 115                 120

cat gag cct cgg act ttt gct gta tat ctt aac aac act ggc tac aga  917
His Glu Pro Arg Thr Phe Ala Val Tyr Leu Asn Asn Thr Gly Tyr Arg
                 125                 130                 135

aca gcc ttt ttt gga aaa tac ctc aat gaa tat aat ggc agc tac atc  965
Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly Ser Tyr Ile
             140                 145                 150

ccc cct ggg tgg cga gaa tgg ctt gga tta atc aag aat tct cgc ttc 1013
Pro Pro Gly Trp Arg Glu Trp Leu Gly Leu Ile Lys Asn Ser Arg Phe
         155                 160                 165

tat aat tac act gtt tgt cgc aat ggc atc aaa gaa aag cat gga ttt 1061
Tyr Asn Tyr Thr Val Cys Arg Asn Gly Ile Lys Glu Lys His Gly Phe
     170                 175                 180

gat tat gca aag gac tac ttc aca gac tta atc act aac gag agc att 1109
Asp Tyr Ala Lys Asp Tyr Phe Thr Asp Leu Ile Thr Asn Glu Ser Ile
185                 190                 195                 200

aat tac ttc aaa atg tct aag aga atg tat ccc cat agg ccc gtt atg 1157
Asn Tyr Phe Lys Met Ser Lys Arg Met Tyr Pro His Arg Pro Val Met
```

8

```
atg gtg atc agc cac gct gcg ccc cac ggc ccc gag gac tca gcc cca   1205
Met Val Ile Ser His Ala Ala Pro His Gly Pro Glu Asp Ser Ala Pro
            220                 225                 230

cag ttt tct aaa ctg tac ccc aat gct tcc caa cac ata act cct agt   1253
Gln Phe Ser Lys Leu Tyr Pro Asn Ala Ser Gln His Ile Thr Pro Ser
            235                 240                 245

tat aac tat gca cca aat atg gat aaa cac tgg att atg cag tac aca   1301
Tyr Asn Tyr Ala Pro Asn Met Asp Lys His Trp Ile Met Gln Tyr Thr
            250                 255                 260

gga cca atg ctg ccc atc cac atg gaa ttt aca aac att cta cag cgc   1349
Gly Pro Met Leu Pro Ile His Met Glu Phe Thr Asn Ile Leu Gln Arg
265                 270                 275                 280

aaa agg ctc cag act ttg atg tca gtg gat gat tct gtg gag agg ctg   1397
Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Val Glu Arg Leu
            285                 290                 295

tat aac atg ctc gtg gag acg ggg gag ctg gag aat act tac atc att   1445
Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Glu Asn Thr Tyr Ile Ile
            300                 305                 310

tac acc gcc gac cat ggt tac cat att ggg cag ttt gga ctg gtc aag   1493
Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly Leu Val Lys
            315                 320                 325

ggg aaa tcc atg cca tat gac ttt gat att cgt gtg cct ttt ttt att   1541
Gly Lys Ser Met Pro Tyr Asp Phe Asp Ile Arg Val Pro Phe Phe Ile
            330                 335                 340

cgt ggt cca agt gta gaa cca gga tca ata gtc cca cag atc gtt ctc   1589
Arg Gly Pro Ser Val Glu Pro Gly Ser Ile Val Pro Gln Ile Val Leu
345                 350                 355                 360

aac att gac ttg gcc ccc acg atc ctg gat att gct ggg ctc gac aca   1637
Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly Leu Asp Thr
            365                 370                 375

cct cct gat gtg gac ggc aag tct gtc ctc aaa ctt ctg gac cca gaa   1685
Pro Pro Asp Val Asp Gly Lys Ser Val Leu Lys Leu Leu Asp Pro Glu
            380                 385                 390

aag cca ggt aac agg ttt cga aca aac aag aag gcc aaa att tgg cgt   1733
Lys Pro Gly Asn Arg Phe Arg Thr Asn Lys Lys Ala Lys Ile Trp Arg
            395                 400                 405

gat aca ttc cta gtg gaa aga ggc aaa ttt cta cgt aag aag gaa gaa   1781
Asp Thr Phe Leu Val Glu Arg Gly Lys Phe Leu Arg Lys Lys Glu Glu
            410                 415                 420

tcc agc aag aat atc caa cag tca aat cac ttg ccc aaa tat gaa cgg   1829
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```
Ser Ser Lys Asn Ile Gln Gln Ser Asn His Leu Pro Lys Tyr Glu Arg
425             430             435             440

gtc aaa gaa cta tgc cag cag gcc agg tac cag aca gcc tgt gaa caa    1877
Val Lys Glu Leu Cys Gln Gln Ala Arg Tyr Gln Thr Ala Cys Glu Gln
                445             450             455

ccg ggg cag aag tgg caa tgc att gag gat aca tct ggc aag ctt cga    1925
Pro Gly Gln Lys Trp Gln Cys Ile Glu Asp Thr Ser Gly Lys Leu Arg
                460             465             470

att cac aag tgt aaa gga ccc agt gac ctg ctc aca gtc cgg cag agc    1973
Ile His Lys Cys Lys Gly Pro Ser Asp Leu Leu Thr Val Arg Gln Ser
                475             480             485

acg cgg aac ctc tac gct cgc ggc ttc cat gac aaa gac aaa gag tgc    2021
Thr Arg Asn Leu Tyr Ala Arg Gly Phe His Asp Lys Asp Lys Glu Cys
        490             495             500

agt tgt agg gag tct ggt tac cgt gcc agc aga agc caa aga aag agt    2069
Ser Cys Arg Glu Ser Gly Tyr Arg Ala Ser Arg Ser Gln Arg Lys Ser
505             510             515             520

caa cgg caa ttc ttg aga aac cag ggg act cca aag tac aag ccc aga    2117
Gln Arg Gln Phe Leu Arg Asn Gln Gly Thr Pro Lys Tyr Lys Pro Arg
                525             530             535

ttt gtc cat act cgg cag aca cgt tcc ttg tcc gtc gaa ttt gaa ggt    2165
Phe Val His Thr Arg Gln Thr Arg Ser Leu Ser Val Glu Phe Glu Gly
                540             545             550

gaa ata tat gac ata aat ctg gaa gaa gaa gaa gaa ttg caa gtg ttg    2213
Glu Ile Tyr Asp Ile Asn Leu Glu Glu Glu Glu Glu Leu Gln Val Leu
                555             560             565

caa cca aga aac att gct aag cgt cat gat gaa ggc cac aag ggg cca    2261
Gln Pro Arg Asn Ile Ala Lys Arg His Asp Glu Gly His Lys Gly Pro
        570             575             580

aga gat ctc cag gct tcc agt ggt ggc aac agg ggc agg atg ctg gca    2309
Arg Asp Leu Gln Ala Ser Ser Gly Gly Asn Arg Gly Arg Met Leu Ala
585             590             595             600

gat agc agc aac gcc gtg ggc cca cct acc act gtc cga gtg aca cac    2357
Asp Ser Ser Asn Ala Val Gly Pro Pro Thr Thr Val Arg Val Thr His
                605             610             615

aag tgt ttt att ctt ccc aat gac tct atc cat tgt gag aga gaa ctg    2405
Lys Cys Phe Ile Leu Pro Asn Asp Ser Ile His Cys Glu Arg Glu Leu
                620             625             630

tac caa tcg gcc aga gcg tgg aag gac cat aag gca tac att gac aaa    2453
Tyr Gln Ser Ala Arg Ala Trp Lys Asp His Lys Ala Tyr Ile Asp Lys
                635             640             645
```

10

```
gag att gaa gct ctg caa gat aaa att aag aat tta aga gaa gtg aga    2501
Glu Ile Glu Ala Leu Gln Asp Lys Ile Lys Asn Leu Arg Glu Val Arg
    650                 655                 660

gga cat ctg aag aga agg aag cct gag gaa tgt agc tgc agt aaa caa    2549
Gly His Leu Lys Arg Arg Lys Pro Glu Glu Cys Ser Cys Ser Lys Gln
665                 670                 675                 680

agc tat tac aat aaa gag aaa ggt gta aaa aag caa gag aaa tta aag    2597
Ser Tyr Tyr Asn Lys Glu Lys Gly Val Lys Lys Gln Glu Lys Leu Lys
                685                 690                 695

agc cat ctt cac cca ttc aag gag gct gct cag gaa gta gat agc aaa    2645
Ser His Leu His Pro Phe Lys Glu Ala Ala Gln Glu Val Asp Ser Lys
            700                 705                 710

ctg caa ctt ttc aag gag aac aac cgt agg agg aag aag gag agg aag    2693
Leu Gln Leu Phe Lys Glu Asn Asn Arg Arg Arg Lys Lys Glu Arg Lys
            715                 720                 725

gag aag aga cgg cag agg aag ggg gaa gag tgc agc ctg cct ggc ctc    2741
Glu Lys Arg Arg Gln Arg Lys Gly Glu Glu Cys Ser Leu Pro Gly Leu
    730                 735                 740

act tgc ttc acg cat gac aac aac cac tgg cag aca gcc ccg ttc tgg    2789
Thr Cys Phe Thr His Asp Asn Asn His Trp Gln Thr Ala Pro Phe Trp
745                 750                 755                 760

aac ctg gga tct ttc tgt gct tgc acg agt tct aac aat aac acc tac    2837
Asn Leu Gly Ser Phe Cys Ala Cys Thr Ser Ser Asn Asn Asn Thr Tyr
                765                 770                 775

tgg tgt ttg cgt aca gtt aat gag acg cat aat ttt ctt ttc tgt gag    2885
Trp Cys Leu Arg Thr Val Asn Glu Thr His Asn Phe Leu Phe Cys Glu
            780                 785                 790

ttt gct act ggc ttt ttg gag tat ttt gat atg aat aca gat cct tat    2933
Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Met Asn Thr Asp Pro Tyr
            795                 800                 805

cag ctc aca aat aca gtg cac acg gta gaa cga ggc att ttg aat cag    2981
Gln Leu Thr Asn Thr Val His Thr Val Glu Arg Gly Ile Leu Asn Gln
    810                 815                 820

cta cac gta caa cta atg gag ctc aga agc tgt caa gga tat aag cag    3029
Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gln Gly Tyr Lys Gln
825                 830                 835                 840

tgc aac cca aga cct aag aat ctt gat gtt gga aat aaa gat gga gga    3077
Cys Asn Pro Arg Pro Lys Asn Leu Asp Val Gly Asn Lys Asp Gly Gly
                845                 850                 855

agc tat gac cta cac aga gga cag tta tgg gat gga tgg gaa ggt taa    3125
Ser Tyr Asp Leu His Arg Gly Gln Leu Trp Asp Gly Trp Glu Gly *
            860                 865                 870
```

11

```
tcagccccgt ctcactgcag acatcaactg gcaaggccta gaggagctac acagtgtgaa 3185
tgaaaacatc tatgagtaca gacaaaacta cagacttagt ctggtggact ggactaatta 3245
cttgaaggat ttagatagag tatttgcact gctgaagagt cactatgagc aaaataaaac 3305
aaataagact caaactgctc aaagtgacgg gttcttggtt gtctctgctg agcacgctgt 3365
gtcaatggag atggcctctg ctgactcaga tgaagaccca aggcataagg ttgggaaaac 3425
acctcatttg accttgccag ctgaccttca aaccctgcat ttgaaccgac caacattaag 3485
tccagagagt aaacttgaat ggaataacga cattccagaa gttaatcatt tgaattctga 3545
acactggaga aaaaccgaaa aatggacggg gcatgaagag actaatcatc tggaaaccga 3605
tttcagtggc gatggcatga cagagctaga gctcgggccc agccccaggc tgcagcccat 3665
tcgcaggcac ccgaaagaac ttccccagta tggtggtcct ggaaaggaca ttttgaaga 3725
tcaactatat cttcctgtgc attccgatgg aatttcagtt catcagatgt tcaccatggc 3785
caccgcagaa caccgaagta attccagcat agcggggaag atgttgacca aggtggagaa 3845
gaatcacgaa aaggagaagt cacagcacct agaaggcagc gcctcctctt cactctcctc 3905
tgattagatg aaactgttac cttaccctaa acacagtatt tctttttaac ttttttattt 3965
gtaaactaat aaaggkaatc acagccacca acattccaag ctaccctggg tacctttgtg 4025
cagtagaagc tagtgagcat gtgagcaagc ggtgtgcaca cggagactca tcgttataat 4085
ttactatctg ccaaggagta gaaagaaagg ctggggatat ttgggttggc tttggktttg 4145
attttttgct tggttggttg gtttgkacta aaacagtatt atcttttgaa tatcgtaggg 4205
acataarkww wwwmmwkktw wtcmawymra kakgsywrra wkgggstyty tskkrkstmw 4265
amwykwscmc cyskkrwwaw tywywmmywc mykytssstg rykrnktaat gaagtt     4321
```

<210> 5
<211> 569
<212> PRT
<213> homo sapiens

<400> 5
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Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly
 1               5                  10                 15
Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro
             20                  25                 30
Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His
             35                  40                 45
Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr
     50                  55                 60
His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys
65                  70                 75                     80
Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser
                 85                 90                 95
Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln
             100                105                110
His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln
             115                120                125
Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met
     130                135                140
Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr
145                150                155                160
Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp
                 165                170                175
Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp
             180                185                190
Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser
             195                200                205
Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser
```

12

```
                210                    215                    220
Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr
225                    230                    235                    240
Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly
                245                    250                    255
Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu
                260                    265                    270
Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn
                275                    280                    285
Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser
                290                    295                    300
Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu
305                    310                    315                    320
Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg
                325                    330                    335
Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro
                340                    345                    350
Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu
                355                    360                    365
Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro
                370                    375                    380
Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln
385                    390                    395                    400
His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln
                405                    410                    415
Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly
                420                    425                    430
Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser
                435                    440                    445
Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu
                450                    455                    460
Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln
465                    470                    475                    480
Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn
                485                    490                    495
Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His
                500                    505                    510
Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu
                515                    520                    525
Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg
                530                    535                    540
Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu
545                    550                    555                    560
Asn Thr Arg Leu Met Ser Gln Arg Ile
                565


<210> 6
<211> 2940
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (334)...(2043)
```

13

<400> 6

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ccacgcgtcc  gcccacgcgt  ccggctgcca  cgccgcgtct  caggctggcc  gggctgagcc      60
ggggaagagg  gagcaaaggc  ggcgcagggc  ctgcgcttag  gcagcgggag  gcagctcggc     120
gcgggcctga  cctccccaga  gcgccccgct  gcggccgagc  agatccggcc  cagccgtccg     180
gcagccagtc  ccggaccaga  cactggaccg  tccccggggg  gcgctgaact  ccctcgcagc     240
atccgagccg  gcgggccggt  ggtgcgccct  gggcgcgcga  ggtggtgagg  ccccaggagc     300
ccggcgcgcc  gggacacgcg  ggccggcttg  gcg atg cac acc ctc act ggc ttc        354
                                        Met His Thr Leu Thr Gly Phe
                                         1               5
```

```
tct ctg gtc agc ctg ctc agc ttc ggc tac ctg tcc tgg gac tgg gcc          402
Ser Leu Val Ser Leu Leu Ser Phe Gly Tyr Leu Ser Trp Asp Trp Ala
            10                  15                  20
```

```
aag ccg agc ttc gtg gcc gac ggg ccc ggg gag gct ggc gag cag ccc          450
Lys Pro Ser Phe Val Ala Asp Gly Pro Gly Glu Ala Gly Glu Gln Pro
        25                  30                  35
```

```
tcg gcc gct ccg ccc cag cct ccc cac atc atc ttc atc ctc acg gac          498
Ser Ala Ala Pro Pro Gln Pro Pro His Ile Ile Phe Ile Leu Thr Asp
40                  45                  50                  55
```

```
gac caa ggc tac cac gac gtg ggc tac cat ggt tca gat atc gag acc          546
Asp Gln Gly Tyr His Asp Val Gly Tyr His Gly Ser Asp Ile Glu Thr
                60                  65                  70
```

```
cct acg ctg gac agg ctg gcg gcc aag ggg gtc aag ttg gag aat tat          594
Pro Thr Leu Asp Arg Leu Ala Ala Lys Gly Val Lys Leu Glu Asn Tyr
                75                  80                  85
```

```
tac atc cag ccc atc tgc acg cct tcg cgg agc cag ctc ctc act ggc          642
Tyr Ile Gln Pro Ile Cys Thr Pro Ser Arg Ser Gln Leu Leu Thr Gly
            90                  95                  100
```

```
agg tac cag atc cac aca gga ctc cag cat tcc atc atc cgc cca cag          690
Arg Tyr Gln Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Gln
105                 110                 115
```

```
cag ccc aac tgc ctg ccc ctg gac cag gtg aca ctg cca cag aag ctg          738
Gln Pro Asn Cys Leu Pro Leu Asp Gln Val Thr Leu Pro Gln Lys Leu
120                 125                 130                 135
```

```
cag gag gca ggt tat tcc acc cat atg gtg ggc aag tgg cac ctg ggc          786
Gln Glu Ala Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly
                140                 145                 150
```

```
ttc tac cgg aag gag tgt ctg ccc acc cgt cgg ggc ttc gac acc ttc          834
Phe Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg Gly Phe Asp Thr Phe
                155                 160                 165
```

```
ctg ggc tcg ctc acg ggc aat gtg gac tat tac acc tat gac aac tgt          882
Leu Gly Ser Leu Thr Gly Asn Val Asp Tyr Tyr Thr Tyr Asp Asn Cys
            170                 175                 180
```

14

```
gat ggc cca ggc gtg tgc ggc ttc gac ctg cac gag ggt gag aat gtg          930
Asp Gly Pro Gly Val Cys Gly Phe Asp Leu His Glu Gly Glu Asn Val
    185                 190                 195

gcc tgg ggg ctc agc ggc cag tac tcc act atg ctt tac gcc cag cgc          978
Ala Trp Gly Leu Ser Gly Gln Tyr Ser Thr Met Leu Tyr Ala Gln Arg
200                 205                 210                 215

gcc agc cat atc ctg gcc agc cac agc cct cag cgt ccc ctc ttc ctc         1026
Ala Ser His Ile Leu Ala Ser His Ser Pro Gln Arg Pro Leu Phe Leu
                220                 225                 230

tat gtg gcc ttc cag gca gta cac aca ccc ctg cag tcc cct cgt gag         1074
Tyr Val Ala Phe Gln Ala Val His Thr Pro Leu Gln Ser Pro Arg Glu
                235                 240                 245

tac ctg tac cgc tac cgc acc atg ggc aat gtg gcc cgg cgg aag tac         1122
Tyr Leu Tyr Arg Tyr Arg Thr Met Gly Asn Val Ala Arg Arg Lys Tyr
            250                 255                 260

gcg gcc atg gtg acc tgc atg gat gag gct gtg cgc aac atc acc tgg         1170
Ala Ala Met Val Thr Cys Met Asp Glu Ala Val Arg Asn Ile Thr Trp
265                 270                 275

gcc ctc aag cgc tac ggt ttc tac aac aac agt gtc atc atc ttc tcc         1218
Ala Leu Lys Arg Tyr Gly Phe Tyr Asn Asn Ser Val Ile Ile Phe Ser
280                 285                 290                 295

agt gac aat ggt ggc cag act ttc tcg ggg ggc agc aac tgg ccg ctc         1266
Ser Asp Asn Gly Gly Gln Thr Phe Ser Gly Gly Ser Asn Trp Pro Leu
                300                 305                 310

cga gga cgc aag ggc act tat tgg gaa ggt ggc gtg cgg ggc cta ggc         1314
Arg Gly Arg Lys Gly Thr Tyr Trp Glu Gly Gly Val Arg Gly Leu Gly
                315                 320                 325

ttt gtc cac agt ccc ctg ctc aag cga aag caa cgg aca agc cgg gca         1362
Phe Val His Ser Pro Leu Leu Lys Arg Lys Gln Arg Thr Ser Arg Ala
            330                 335                 340

ctg atg cac atc act gac tgg tac ccg acc ctg gtg ggt ctg gca ggt         1410
Leu Met His Ile Thr Asp Trp Tyr Pro Thr Leu Val Gly Leu Ala Gly
        345                 350                 355

ggt acc acc tca gca gcc gat ggg cta gat ggc tac gac gtg tgg ccg         1458
Gly Thr Thr Ser Ala Ala Asp Gly Leu Asp Gly Tyr Asp Val Trp Pro
360                 365                 370                 375

gcc atc agc gag ggc cgg gcc tca cca cgc acg gag atc ctg cac aac         1506
Ala Ile Ser Glu Gly Arg Ala Ser Pro Arg Thr Glu Ile Leu His Asn
                380                 385                 390

att gac cca ctc tac aac cat gcc cag cat ggc tcc ctg gag ggc ggc         1554
Ile Asp Pro Leu Tyr Asn His Ala Gln His Gly Ser Leu Glu Gly Gly
                395                 400                 405
```

15

```
ttt ggc atc tgg aac acc gcc gtg cag gct gcc atc cgc gtg ggt gag      1602
Phe Gly Ile Trp Asn Thr Ala Val Gln Ala Ala Ile Arg Val Gly Glu
        410                 415                 420

tgg aag ctg ctg aca gga gac ccc ggc tat ggc gat tgg atc cca ccg      1650
Trp Lys Leu Leu Thr Gly Asp Pro Gly Tyr Gly Asp Trp Ile Pro Pro
        425                 430                 435

cag aca ctg gcc acc ttc ccg ggt agc tgg/tgg aac ctg gaa cga atg      1698
Gln Thr Leu Ala Thr Phe Pro Gly Ser Trp Trp Asn Leu Glu Arg Met
440                 445                 450                 455

gcc agt gtc cgc cag gcc gtg tgg ctc ttc aac atc agt gct gac cct      1746
Ala Ser Val Arg Gln Ala Val Trp Leu Phe Asn Ile Ser Ala Asp Pro
                460                 465                 470

tat gaa cgg gag gac ctg gct ggc cag cgg cct gat gtg gtc cgc acc      1794
Tyr Glu Arg Glu Asp Leu Ala Gly Gln Arg Pro Asp Val Val Arg Thr
            475                 480                 485

ctg ctg gct cgc ctg gcc gaa tat aac cgc aca gcc atc ccg gta cgc      1842
Leu Leu Ala Arg Leu Ala Glu Tyr Asn Arg Thr Ala Ile Pro Val Arg
        490                 495                 500

tac cca gct gag aac ccc cgg gct cat cct gac ttt aat ggg ggt gct      1890
Tyr Pro Ala Glu Asn Pro Arg Ala His Pro Asp Phe Asn Gly Gly Ala
        505                 510                 515

tgg ggg ccc tgg gcc agt gat gag gaa gag gag gaa gag gaa ggg agg      1938
Trp Gly Pro Trp Ala Ser Asp Glu Glu Glu Glu Glu Glu Glu Gly Arg
520                 525                 530                 535

gct cga agc ttc tcc cgg ggt cgt cgc aag aaa aaa tgc aag att tgc      1986
Ala Arg Ser Phe Ser Arg Gly Arg Arg Lys Lys Lys Cys Lys Ile Cys
                540                 545                 550

aag ctt cga tcc ttt ttc cgt aaa ctc aac acc agg cta atg tcc caa      2034
Lys Leu Arg Ser Phe Phe Arg Lys Leu Asn Thr Arg Leu Met Ser Gln
                555                 560                 565

cgg atc tga tggtggggag ggagaaaact gtcctttaga ggatcttccc            2083
Arg Ile  *

cactccggct tggccctgct gtttctcagg gagaagcctg tcacatctcc atctacaggg   2143
agttggaggg tgtagagtcc cttggttgaa cagggtaggg agcctggata ggagtgggtg   2203
ggaataaacc agactgggat gcctgtgtct cagtcctgcc tcctcacgga cttgctctgt   2263
gacctcaggt gacccacatg agcttttagc ctcagtttcc tcatctgtaa aatgagctct   2323
aatgactttg tgactctttg gtgtggccct ggagcctggg gccacggtgg agttcctggc   2383
cggccttgcc acttgacaac tcctttaagg cttccccctt aacacgggat ccctgtggtg   2443
gtgtttggga gttgcctgga ggcaactcca agcctggccc ccagctgaag catggcaatc   2503
tggctgctct ctacagggac ccccaagcgc tgtgggtgga gggcagggt cggggggtt    2563
gaccttcttg ggtcttcaca tggcctaggc cagtcctccg gtcagactgg tgtcaggcac   2623
cgtggtgcaa aattcctctt ctggcccctc cagtacccag agaaactggc tgggccatta   2683
```

16

```
actgctgcag caccaagggt ggtagaaaga gctgtgaaga gccccaaac cagtaccagg    2743
acacctgggt tctcctgtga cctggggcac agttcttgcc ctctaggcct tgatttcccc    2803
acctgcaagt ggggatgcca gccctggctc tgcctccttc atgaggctct ggaagactgg    2863
ccaaggttgt ggaggagctt gtgaacttga ttaaagtgtc gtaacatgga aaaaaaaaa     2923
aaaaaaaaaa agggcgg                                                   2940
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<210> 7
<211> 550
<212> PRT
<213> homo sapiens

<400> 7

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Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro Gln
 1               5                  10                  15
Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu Ala Gly
            20                  25                  30
Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser Trp Gly Gln
        35                  40                  45
Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala Gln Ala Gly Glu
    50                  55                  60
Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln Pro His Leu Ile Phe
65                  70                  75                  80
Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp Val Gly Tyr His Gly Ser
                85                  90                  95
Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu Ala Ala Glu Gly Val Lys
            100                 105                 110
Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys Thr Pro Ser Arg Ser Gln
            115                 120                 125
Phe Ile Thr Gly Lys Tyr Gln Ile His Thr Gly Leu Gln His Ser Ile
    130                 135                 140
Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu
145                 150                 155                 160
Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met Val Gly Lys
                165                 170                 175
Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Met Pro Thr Arg Arg Gly
            180                 185                 190
Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr
            195                 200                 205
His Tyr Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu
    210                 215                 220
Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln
225                 230                 235                 240
Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro Thr
                245                 250                 255
Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln Ala Val His Ser Pro Leu
            260                 265                 270
Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile Ile Asn Ile
            275                 280                 285
Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu Asp Glu Ala Ile
    290                 295                 300
Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly Phe Tyr Asn Asn Ser
305                 310                 315                 320
Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly Gln Pro Thr Ala Gly Gly
                325                 330                 335
Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly Thr Tyr Trp Glu Gly Gly
```

17

```
                    340                      345                      350
   Ile Arg Ala Val Gly Phe Val His Ser Pro Leu Leu Lys Asn Lys Gly
            355                      360                      365
   Thr Val Cys Lys Glu Pro Val His Ile Thr Asp Trp Tyr Pro Thr Leu
            370                      375                      380
   Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly
   385                      390                      395                      400
   Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val
                         405                      410                      415
   Asp Ile Leu His Asn Ile Asp Pro Ile Tyr Thr Lys Ala Lys Asn Gly
            420                      425                      430
   Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn Thr Ala Ile Gln Ser Ala
            435                      440                      445
   Ile Arg Val Gln His Trp Lys Leu Leu Thr Gly Asn Pro Gly Tyr Ser
            450                      455                      460
   Asp Trp Val Pro Pro Gln Ser Phe Ser Asn Leu Gly Pro Asn Arg Trp
   465                      470                      475                      480
   His Asn Glu Arg Ile Thr Ser Ser Thr Gly Lys Ser Val Trp Leu Phe
                         485                      490                      495
   Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val Asp Leu Ser Asn Arg Tyr
            500                      505                      510
   Pro Gly Ile Val Lys Lys Leu Leu Arg Arg Leu Ser Gln Phe Asn Lys
            515                      520                      525
   Thr Ala Val Pro Val Arg Tyr Pro Pro Lys Asp Pro Arg Ser Asn Pro
            530                      535                      540
   Arg Leu Asn Gly Gly Val
   545                      550
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<210> 8
<211> 2266
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (324)...(1977)

<400> 8
cacgcgtccg cccacgcgtc cgtggagata ttaactttt tctttttttt tttccttggt 60
ggaagctgct ctagggaggg gggaggagga ggagaaagtg aaatgtgctg gagaagagcg 120
agccctcctt gttcttccgg agtcccatcc attaagccat cacttctgga agattaaagt 180
tgtcggacat ggtgacagct gagaggagag gaggatttct tgccaggtgg agagtcttca 240
ccgtctgttg ggtgcatgtg tgcgcccgca scggcgcggg gcgcgtggtt ctccgcgtgg 300
agtctcacct gggacctgag tga atg gct ccc agg ggc tgt gcg ggg cat ccg 353
                         Met Ala Pro Arg Gly Cys Ala Gly His Pro
                          1               5                    10

cct ccg cct tct cca cag gcc tgt gtc tgt cct gga aag atg cta gca     401
Pro Pro Pro Ser Pro Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala
                 15              20                      25

atg ggg gcg ctg gca gga ttc tgg atc ctc tgc ctc ctc act tat ggt     449
Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly
             30                      35                      40
```

18

```
tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta        497
Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu
            45                  50                  55

cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc        545
Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser
    60                  65                  70

cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat       593
Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
75                  80                  85                  90

gtg ggt tac cac gga tct gag att aaa aca cct act ctt gac aag ctc       641
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu
                    95                  100                 105

gct gcc gaa gga gtt aaa ctg gag aac tac tat gtc cag cct att tgc       689
Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys
                110                 115                 120

aca cca tcc agg agt cag ttt att act gga aag tat cag ata cac acc       737
Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr
            125                 130                 135

gga ctt caa cat tct atc ata aga cct acc caa ccc aac tgt tta cct       785
Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro
        140                 145                 150

ctg gac aat gcc acc cta cct cag aaa ctg aag gag gtt gga tat tca       833
Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser
155                 160                 165                 170

acg cat atg gtc gga aaa tgg cac ttg ggt ttt tac aga aaa gaa tgc       881
Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys
                    175                 180                 185

atg ccc acc aga aga gga ttt gat acc ttt ttt ggt tcc ctt ttg gga       929
Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly
                190                 195                 200

agt ggg gat tac tat aca cac tac aaa tgt gac agt cct ggg atg tgt       977
Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys
            205                 210                 215

ggc tat gac ttg tat gaa aac gac aat gct gcc tgg gac tat gac aat      1025
Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn
    220                 225                 230

ggc ata tac tcc aca cag atg tac act cag aga gta cag caa atc tta      1073
Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu
235                 240                 245                 250

gct tcc cat aac ccc aca aag cct ata ttt tta tat att gcc tat caa      1121
Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln
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gct gtt cat tca cca ctg caa gct cct ggc agg tat ttc gaa cac tac    1169
Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr
            270             275             280

cga tcc att atc aac ata aac agg agg aga tat gct gcc atg ctt tcc    1217
Arg Ser Ile Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser
            285             290             295

tgc tta gat gaa gca atc aac aac gtg aca ttg gct cta aag act tat    1265
Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr
    300             305             310

ggt ttc tat aac aac agc att atc att tac tct tca gat aat ggt ggc    1313
Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
315             320             325             330

cag cct acg gca gga ggg agt aac tgg cct ctc aga ggt agc aaa gga    1361
Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly
            335             340             345

aca tat tgg gaa gga ggg atc cgg gct gta ggc ttt gtg cat agc cca    1409
Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro
            350             355             360

ctt ctg aaa aac aag gga aca gtg tgt aag gaa cct gtg cac atc act    1457
Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Pro Val His Ile Thr
            365             370             375

gac tgg tac ccc act ctc att tca ctg gct gaa gga cag att gat gag    1505
Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu
    380             385             390

gac att caa cta gat ggc tat gat atc tgg gag acc ata agt gag ggt    1553
Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly
395             400             405             410

ctt cgc tca ccc cga gta gat att ttg cat aac att gac ccc ata tac    1601
Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr
            415             420             425

acc aag gca aaa aat ggc tcc tgg gca gca ggc tat ggg atc tgg aac    1649
Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn
            430             435             440

act gca atc cag tca gcc atc aga gtg cag cac tgg aaa ttg ctt aca    1697
Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr
            445             450             455

gga aat cct ggc tac agc gac tgg gtc ccc cct cag tct ttc agc aac    1745
Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn
            460             465             470

ctg gga ccg aac cgg tgg cac aat gaa cgg atc acc tcg tca act ggc    1793
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Leu Gly Pro ??? Arg Trp His Asn Glu Arg Ile Thr Ser Ser Thr Gly
475             480             485             490

aaa agt gta tgg ctt ttc aac atc aca gcc gac cca tat gag agg gtg    1841
Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val
                495             500             505

gac cta tct aac agg tat cca gga atc gtg aag aag ctc cta cgg agg    1889
Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg
            510             515             520

ctc tca cag ttc aac aaa act gca gtg ccg gtc agg tat ccc ccc aaa    1937
Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys
        525             530             535

gac ccc aga agt aac cct agg ctc aat gga ggg gtc tag g gaccatggta    1987
Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val *
    540             545             550

tagagaggaa accaagaaaa agaagccaag caaaaatcag gctgagaaaa agcaaaagaa    2047
aagcaaaaaa agaagaagaa acagcagaaa gcagtctcag gttcaacttg ccattcaggt    2107
gttacttgtg gataagcaca aatatttcct gtttggttaa actttaatca gttcttatct    2167
ttcatctgtt tcctaggtaa accagcaaat ttggctcgat aatatcgctg gcctaagcgt    2227
caggcttgtt ttcatgctgt gccacctggt gccgaattc                          2266
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